

K. Canella  
09/531369

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/531,369

DATE: 09/14/2000  
TIME: 10:25:28

Input Set : A:\Sequence.txt  
Output Set: N:\CRF3\09142000\I531369.raw

4 <110> APPLICANT: Williamson, Mark  
6 <120> TITLE OF INVENTION: MDA-9 AND USES THEREOF  
8 <130> FILE REFERENCE: 07334-122001  
10 <140> CURRENT APPLICATION NUMBER: US 09/531,369  
C--> 11 <141> CURRENT FILING DATE: 1999-03-21  
13 <150> PRIOR APPLICATION NUMBER: US 60/125,759  
14 <151> PRIOR FILING DATE: 1999-03-23  
16 <160> NUMBER OF SEQ ID NOS: 3  
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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21 <211> LENGTH: 2068  
22 <212> TYPE: DNA  
23 <213> ORGANISM: Homo sapiens  
25 <220> FEATURE:  
26 <221> NAME/KEY: CDS  
27 <222> LOCATION: (76)...(970)  
29 <400> SEQUENCE: 1  
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31 aagaatcccg caaaa atg tct ctc tat cca tct ctc gaa gac ttg aag gta 111  
32 Met Ser Leu Tyr Pro Ser Leu Glu Asp Leu Lys Val  
33 1 5 10  
35 gac aaa gta att cag gct caa act gct ttt tct gca aac cct gcc aat 159  
36 Asp Lys Val Ile Gln Ala Gln Thr Ala Phe Ser Ala Asn Pro Ala Asn  
37 15 20 25  
39 cca gca att ttg tca gaa gct tct gct cct atc cct cac gat gga aat 207  
40 Pro Ala Ile Leu Ser Glu Ala Ser Ala Pro Ile Pro His Asp Gly Asn  
41 30 35 40  
43 ctc tat ccc aga ctg tat cca gag ctc tct caa tac atg ggg ctg agt 255  
44 Leu Tyr Pro Arg Leu Tyr Pro Glu Leu Ser Gln Tyr Met Gly Leu Ser  
45 45 50 55 60  
47 tta aat gaa gaa gaa ata cgt gca aat gtg gcc gtg gtt tct ggt gca 303  
48 Leu Asn Glu Glu Glu Ile Arg Ala Asn Val Ala Val Val Ser Gly Ala  
49 65 70 75  
51 cca ctt cag ggg cag ttg gta gca aga cct tcc agt ata aac tat atg 351  
52 Pro Leu Gln Gly Gln Leu Val Ala Arg Pro Ser Ser Ile Asn Tyr Met  
53 80 85 90  
55 gtg gct cct gta act ggt aat gat gtt gga att cgt aga gca gaa att 399  
56 Val Ala Pro Val Thr Gly Asn Asp Val Gly Ile Arg Arg Ala Glu Ile  
57 95 100 105  
59 aag caa ggg att cgt gaa gtc att ttg tgt aag gat caa gat gga aaa 447  
60 Lys Gln Gly Ile Arg Glu Val Ile Leu Cys Lys Asp Gln Asp Gly Lys  
61 110 115 120  
63 att gga ctc agg ctt aaa tca ata gat aat ggt ata ttt gtt cag cta 495  
64 Ile Gly Leu Arg Leu Lys Ser Ile Asp Asn Gly Ile Phe Val Gln Leu  
65 125 130 135 140  
67 gtc cag gct aat tct cca gcc tca ttg gtt ggt ctg aga ttt ggg gac 543  
68 Val Gln Ala Asn Ser Pro Ala Ser Leu Val Gly Leu Arg Phe Gly Asp

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69          145          150          155
71 caa gta ctt cag atc aat ggt gaa aac tgt gca gga tgg agc tct gat 591
72 Gln Val Leu Gln Ile Asn Gly Glu Asn Cys Ala Gly Trp Ser Ser Asp
73          160          165          170
75 aaa gcg cac aag gtg ctc aaa cag gct ttt gga gag aag att acc atg 639
76 Lys Ala His Lys Val Leu Lys Gln Ala Phe Gly Glu Lys Ile Thr Met
77          175          180          185
79 acc att cgt gac agg ccc ttt gaa cgg acg att acc atg cat aag gat 687
80 Thr Ile Arg Asp Arg Pro Phe Glu Arg Thr Ile Thr Met His Lys Asp
81          190          195          200
83 agc act gga cat gtt ggt ttt atc ttt aaa aat gga aaa ata aca tcc 735
84 Ser Thr Gly His Val Gly Phe Ile Phe Lys Asn Gly Lys Ile Thr Ser
85 205          210          215          220
87 ata gtg aaa gat agc tct gca gcc aga aat ggt ctt ctc acg gaa cat 783
88 Ile Val Lys Asp Ser Ser Ala Ala Arg Asn Gly Leu Leu Thr Glu His
89          225          230          235
91 aac atc tgt gaa atc aat gga cag aat gtc att gga ttg aag gac tct 831
92 Asn Ile Cys Glu Ile Asn Gly Gln Asn Val Ile Gly Leu Lys Asp Ser
93          240          245          250
95 caa att gca gac ata ctg tca aca tct ggg act gta gtt act att aca 879
96 Gln Ile Ala Asp Ile Leu Ser Thr Ser Gly Thr Val Val Thr Ile Thr
97          255          260          265
99 atc atg cct gct ttt atc ttt gaa cat att att aag cgg atg gca cca 927
100 Ile Met Pro Ala Phe Ile Phe Glu His Ile Ile Lys Arg Met Ala Pro
101          270          275          280
103 agc att atg aaa agc cta atg gac cac acc att cct gag gtt t 970
W--> 104 Ser Ile Met Lys Ser Leu Met Asp His Thr Ile Pro Glu Val
105 285          290          295
107 aaaattcacg gcaccatgga aatgtagctg aacgtctcca gtttccttct ttggcaactt 1030
108 ctgtattatg cacgtgaagc cttcccggag ccagcgagca tatgctgcat gaggaccttt 1090
109 ctatcttaca ttatggctgg gaatcttact ctttcactcg ataccttgtt cagatttcaa 1150
110 aatagttgta gccttatcct ggttttacag atgtgaaact ttcaaagatg ttactgactt 1210
111 tcttagaata gtttctctac tggaaaacctg atgcttttat aagccattgt gattaggatg 1270
112 actgttacag gcttagcttt gtgtgaaaac cagtcacott tctcttaggt aatgagtagt 1330
113 gctgttcata ttacttttagt tctatagcat actgcatctt taacatgcta tcatagtaca 1390
114 tttagaatga ttgcctttga tttttttttt aaattctgtg tgtgtgtgtg taaaatgcca 1450
115 attaagaaca ctggtttcat tccatgtaag cattaaacag tgtatgtagg tttcaagaga 1510
116 ttgtgatgat tcttaaatat taactacott cacttaatat gcttgaactg tcgccttaac 1570
117 tatgttaagc atctagacta aaagccaaaa tataattatt gctgcctttc taaaaaccca 1630
118 aaatgtagtt ctctattaac ctgaaatgta cactagccca gaacagttaa atggtactta 1690
119 ctgagctata gcatagctgc ttagtgtgtt ttgagagttt ttagtcaaca cataatggaa 1750
120 acttctttct tctaaaagtt gccagtgccca cttttaagaa gtgaatcact atatgtgatg 1810
121 taaaagttat tacactaaac aggataaact tttagactccc cttttgttca tttgtggatt 1870
122 aagtgggata atacttaatt ttggcatttg actccttaaga ttatgtaacc tagctacttt 1930
123 gggatgggtct tagaatatatt ttctgataac ttgttccttt tctgtactcc tccttgcaaa 1990
124 caaaatgata gttgacactt tatectgatt tttttcttct ttttggttta tgtctattct 2050
125 aattaaatat gtataaat
127 <210> SEQ ID NO: 2
128 <211> LENGTH: 298

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129 <212> TYPE: PRT
130 <213> ORGANISM: Homo sapiens
132 <400> SEQUENCE: 2
133 Met Ser Leu Tyr Pro Ser Leu Glu Asp Leu Lys Val Asp Lys Val Ile
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135 Gln Ala Gln Thr Ala Phe Ser Ala Asn Pro Ala Asn Pro Ala Ile Leu
136 20 25 30
137 Ser Glu Ala Ser Ala Pro Ile Pro His Asp Gly Asn Leu Tyr Pro Arg
138 35 40 45
139 Leu Tyr Pro Glu Leu Ser Gln Tyr Met Gly Leu Ser Leu Asn Glu Glu
140 50 55 60
141 Glu Ile Arg Ala Asn Val Ala Val Val Ser Gly Ala Pro Leu Gln Gly
142 65 70 75 80
143 Gln Leu Val Ala Arg Pro Ser Ser Ile Asn Tyr Met Val Ala Pro Val
144 85 90 95
145 Thr Gly Asn Asp Val Gly Ile Arg Arg Ala Glu Ile Lys Gln Gly Ile
146 100 105 110
147 Arg Glu Val Ile Leu Cys Lys Asp Gln Asp Gly Lys Ile Gly Leu Arg
148 115 120 125
149 Leu Lys Ser Ile Asp Asn Gly Ile Phe Val Gln Leu Val Gln Ala Asn
150 130 135 140
151 Ser Pro Ala Ser Leu Val Gly Leu Arg Phe Gly Asp Gln Val Leu Gln
152 145 150 155 160
153 Ile Asn Gly Glu Asn Cys Ala Gly Trp Ser Ser Asp Lys Ala His Lys
154 165 170 175
155 Val Leu Lys Gln Ala Phe Gly Glu Lys Ile Thr Met Thr Ile Arg Asp
156 180 185 190
157 Arg Pro Phe Glu Arg Thr Ile Thr Met His Lys Asp Ser Thr Gly His
158 195 200 205
159 Val Gly Phe Ile Phe Lys Asn Gly Lys Ile Thr Ser Ile Val Lys Asp
160 210 215 220
161 Ser Ser Ala Ala Arg Asn Gly Leu Leu Thr Glu His Asn Ile Cys Glu
162 225 230 235 240
163 Ile Asn Gly Gln Asn Val Ile Gly Leu Lys Asp Ser Gln Ile Ala Asp
164 245 250 255
165 Ile Leu Ser Thr Ser Gly Thr Val Val Thr Ile Thr Ile Met Pro Ala
166 260 265 270
167 Phe Ile Phe Glu His Ile Ile Lys Arg Met Ala Pro Ser Ile Met Lys
168 275 280 285
169 Ser Leu Met Asp His Thr Ile Pro Glu Val
170 290 295
172 <210> SEQ ID NO: 3
173 <211> LENGTH: 894
174 <212> TYPE: DNA
175 <213> ORGANISM: Homo sapiens
177 <400> SEQUENCE: 3
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179 gctttttctg caaacctgc caatccagca attttgtcag aagcttctgc tcctatccct 120
180 cacgatggaa atctctatcc cagactgtat ccagagctct ctcaatacat ggggctgagt 180

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181	ttaaatgaag	aagaaatacg	tgcaaatgtg	gccgtgggtt	ctgggtgcacc	acttcagggg	240
182	cagttggtag	caagaccttc	cagtataaac	tatatgggtg	ctcctgtaac	tggtaatgat	300
183	gttgggaattc	gtagagcaga	aattaagcaa	gggattcgtg	aagtcatttt	gtgtaaggat	360
184	caagatggaa	aaattggact	caggccttaa	tcaatagata	atggatatatt	tggtcagcta	420
185	gtccaggcta	attctccagc	ctcattgggt	ggtctgagat	ttggggacca	agtacttcag	480
186	atcaatggtg	aaaactgtgc	aggatggagc	tctgataaa	gcacacaagg	gtcacaacag	540
187	gcttttggtg	agaagattac	catgaccatt	cgtgacaggc	cctttgaacg	gacgattacc	600
188	atgcataagg	atagcactgg	acatgttggt	tttatcttta	aaaatggaaa	aataacatcc	660
189	atagtgaag	atagctctgc	agccagaaat	ggtcttctca	cggaacataa	catctgtgaa	720
190	atcaatggac	agaatgtcat	tggattgaag	gactctcaaa	ttgcagacat	actgtcaaca	780
191	tctggggactg	tagttactat	tacaatcatg	cctgctttta	tctttgaaca	tattattaag	840
192	cggtatggcac	caagcattat	gaaaagccta	atggaccaca	ccattcctga	ggtt	894

VERIFICATION SUMMARY  
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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:104 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 1

Application No.:

09/53/389

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☒ 6. ~~The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).~~
- ☐ 7. Other: \_\_\_\_\_

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

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